

**SEARCH REQUEST FORM**

Scientific and Technical Information Center

Requester's Full Name: Bruce William Tedeschi Examiner #: 78150 Date: 2/1/01  
 Art Unit: 1642 Phone Number 306-4823 Serial Number: 09/481990  
 Mail Box and Bldg/Room Location: CM1/Room Results Format Preferred (circle): PAPER DISK E-MAIL

**If more than one search is submitted, please prioritize searches in order of need.**

\*\*\*\*\*

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: FAMILY OF MAMMALIAN POTASSIUM channels, Their cloning

Inventors (please provide full names): FLORIAN LISAGE, ERIC GUILLEMARE, Michael FINK, Fabrice DUPONT, et al.

Earliest Priority Filing Date: Jan 11, 2000

*\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

SEQ ID# 1

SEQ ID# 2

**STAFF USE ONLY**

Searcher: B. Smith  
 Searcher Phone #: 308-41177  
 Searcher Location: CM1-1E7  
 Date Searcher Picked Up: 2/2/01  
 Date Completed: 2/21/01  
 Searcher Prep & Review Time: \_\_\_\_\_  
 Clerical Prep Time: 3  
 Online Time: \_\_\_\_\_

**Type of Search**

NA Sequence (#) 1  
 AA Sequence (#) 1  
 Structure (#) \_\_\_\_\_  
 Bibliographic \_\_\_\_\_  
 Litigation \_\_\_\_\_  
 Fulltext \_\_\_\_\_  
 Patent Family \_\_\_\_\_  
 Other \_\_\_\_\_

**Vendors and cost where applicable**

STN \_\_\_\_\_  
 Dialog \_\_\_\_\_  
 Questel/Orbit \_\_\_\_\_  
 Dr.Link \_\_\_\_\_  
 Lexis/Nexis \_\_\_\_\_  
 Sequence Systems abss03  
 WWW/Internet \_\_\_\_\_  
 Other (specify) abss04

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 13, 2001, 18:54:41 : Search time 2260.72 Seconds  
(without alignments)  
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Scoring table: IDENTITY-NOC  
Gapop 10.0 , Gapext 1.0

Searched: 118133 seqs, 2558875100 residues

Total number of hits satisfying chosen parameters: 2236266

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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85: gb\_pr8:\*

Pred. No. is the number of results predicted by chance to have a  
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and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1882	99.4	1882	53	HSU33632
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## ALIGNMENTS

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 LOCUS Human two P-domain K+ channel TWIK-1 mRNA, complete cds.  
 DEFINITION U33632  
 ACCESSION U33632  
 VERSION U33632.1 GI:1086490  
 KEYWORDS

## SOURCE

ORGANISM human.  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

## REFERENCE

Lesage, F., Guillemaire, E., Fink, M., Duprat, F., Lazdunski, M.,  
 Romey, G. and Barhanin, J.  
 TWIK-1, a ubiquitous human weakly inward rectifying K+ channel with  
 a novel structure  
 EMBO J. 15 (5), 1004-1011 (1996)

## JOURNAL

6183184  
 2 (bases 1 to 1882)

## AUTHORS

Lesage, F.

Direct Submission  
 Submitted (11-AUG-1995) Florian Lesage, Institut de Pharmacologie  
 Moléculaire et Cellulaire-CNRS, 660 Route des Lucioles, Valbonne  
 06560, France

## TITLE

## JOURNAL

## FEATURES

## Source

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RESULT 2  
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 ACCESSION U76996.1 GI:281119

KEYWORDS  
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 ORGANISM Homo sapiens  
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 REFERENCE  
 AUTHORS Goldstein, S.A., Wang, K.W., Ilan, N. and Pausch, M.H.  
 TITLE Sequence and function of the two P domain potassium channels:  
 implications of an emerging superfamily  
 J. Mol. Med. 76 (1), 13-20 (1998)  
 JOURNAL 98122696  
 MEDLINE 2 (bases 1 to 1860)  
 REFERENCE Goldstein, S.A.N.  
 AUTHORS Direct Submission  
 TITLE Submitted (01-NOV-1996) Departments of Pediatrics and Cellular and  
 Molecular Physiology, Yale University School of Medicine, Boyer  
 Center for Molecular Medicine, 295 Congress Avenue, New Haven, CT  
 06536, USA  
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Db	1563	TATGACATATAAAGTATAAATATGTTTATATTTCTGCATATAGGTTTAAAGTACCACAT	1622
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RESULT	3		
LOCUS	HSU90065	1224 bp	mRNA
DEFINITION	Human potassium channel KCNO1 mRNA, complete cds.		
ACCESSION	U90065		
VERSION	U90065.1	GI:1916294	
KEYWORDS	human.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 1224)		
TITLE	Desir,G.V., Orlas,M. and Freeman,T.		
JOURNAL	The cloning of a human potassium channel with two pores unpublished		
REFERENCE	2 (bases 1 to 1224)		
AUTHORS	Desir,G.V., Orlas,M. and Freeman,T.		
TITLE	Direct Submission		
JOURNAL	Submitted (19-FEB-1997) Internal Medicine, Yale University, 333 Cedar St., New Haven, CT 06610, USA		
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Matches 1224;	Conservative 0;	Mismatches 0;	Gaps 0;
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LOCUS Mus musculus TWIK-1 K+ channel mRNA, complete cds.
ACCESSION AF033017 086009
VERSION AF033017.1 GI:3150442
KEYWORDS house mouse.
SOURCE Mus musculus.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2240)
Lesage, F., Lauritzen, I., Duprat, F., Reyes, R., Fink, M., Heurteaux, C.
and Lazdunski, M.
The structure, function and distribution of the mouse TWIK-1 K+
channel
FEBS Lett. 402 (1), 28-32 (1997)
MEDLINE 97165959
REFERENCE 2 (bases 1 to 2240)
Arrighi, I., Lesage, F., Scimeca, J.C., Carle, G.F. and Barhanin, J.
Structure, chromosome localization, and tissue distribution of the
mouse twik K+ channel gene
FEBS Lett. 425 (2), 310-316 (1998)
MEDLINE 98218573
REFERENCE 3 (bases 1 to 2240)
Arrighi, I., Lesage, F. and Barhanin, J.
Direct Submission
Submitted (05-NOV-1997) IPWC, CNRS, 660 route des Lucioles,
Valbonne 06560, France
On May 23, 1998 this sequence version replaced gi:1916868.
JOURNAL Location/Qualifiers
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DH"
BASE COUNT 530 a 574 c 579 g 556 t 1 others
ORIGIN

Query Match 53.1%; Score 1005.6; DB 11; Length 2240;
Best Local Similarity 78.8%; Pred. No. 2.5e-134;
Matches 1379; Conservative 0; Mismatches 295; Indels 77; Gaps 12;
QY 158 GGCCTTGGCGGGGGGGGGGAGAAAGATGCTGACGACCCCGCGCGGAGCTGCTGCTGCTGCTGCTGCTGCT 217
Db 266 GGGCGGGAGCGCGGGGGGGGAGATGCTGACGTCCTGCGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 325
QY 218 CCTGTGAGAGCGGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 277
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RESULT 5
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DEFINITION
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VERSION HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE 1 (bases 1 to 119793)
AUTHORS Donnelly, S.
TITLE Direct Submission
JOURNAL Submitted (04-OCT-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
COMMENT On Oct 6, 2000 this sequence version replaced gi:10045423.
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
Project Information
Center project name: dj550F15
Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator ET-amersham; 29% of reads
Dye-terminator Big Dye; 70% of reads
Consensus quality: 119154 bases at least Q40

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[illegible]

Klein, J., Laroque, K., Lamazeres, R., Landers, T., Lehoczy, J., Levine, R., Lieu, C., Liu, G., Locke, K., McDonald, P., Marquis, N., McCarthy, M., McEwan, P., McGill, A., McKenna, K., McPheters, R., Miedema, T., Meneus, L., Minova, T., Miranda, C., Mlenaga, V., Morrow, Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, T. M., Oliver, J., Peterson, K., Pierre, N., Pisaní, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.

TITLE  
JOURNAL  
COMMENT

Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,  
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,  
Tessier, S., Theodores, J., Tirrell, A., Travers, M., Trigilio, J.,  
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,  
Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission  
Submitted (16-MAR-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On May 28, 2000 this sequence version replaced gi:7651989.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www.seq.wi.mit.edu

Contact: sequence\_submissions@genome.wi.mit.edu

----- Project Information

Center project name: 274\_P-19

Center clone name: L8005

----- Summary Statistics

Sequencing vector: M13: M77815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 160532 bases at least Q40

Consensus quality: 16189 bases at least Q30

Consensus quality: 168374 bases at least Q20

Insert size: 171000; agarose-gel

Quality coverage: 4.1 in Q20 bases; agarose-gel

Quality coverage: 4.2 in Q20 bases; sum-of-coverage

----- NOTE: This is a 'working draft' sequence. It currently  
\* consists of 23 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

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* 1172 1271: gap of 100 bp
* 1272 2617: contig of 1346 bp in length
* 2618 2717: gap of 100 bp
* 2718 4098: contig of 1381 bp in length
* 4099 4198: gap of 100 bp
* 4199 6035: contig of 1837 bp in length
* 6036 6135: gap of 100 bp
* 6136 8540: contig of 2405 bp in length
* 8541 8640: gap of 100 bp
* 8641 11132: contig of 2492 bp in length
* 11133 11232: gap of 100 bp
* 11233 14867: contig of 3635 bp in length
* 14868 14967: gap of 100 bp
* 14968 17745: contig of 2778 bp in length
* 17746 17845: gap of 100 bp
* 17846 18890: contig of 1045 bp in length
* 18891 18990: gap of 100 bp
* 18991 21784: contig of 2794 bp in length
* 21785 21884: gap of 100 bp
* 21885 25348: contig of 3464 bp in length
* 25349 25448: gap of 100 bp
* 25449 31428: contig of 5980 bp in length
* 31429 31528: gap of 100 bp
* 31529 38131: contig of 6603 bp in length
* 38132 38231: gap of 100 bp
* 38232 44571: contig of 6340 bp in length
* 44572 44671: gap of 100 bp
* 44672 50542: contig of 5871 bp in length
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* 50643 60925: contig of 10283 bp in length
* 60926 61025: gap of 100 bp
* 61026 71074: contig of 10049 bp in length

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FEATURES  
source

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* 71075 71174: gap of 100 bp
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* 82409 92547: contig of 10139 bp in length
* 92548 92647: gap of 100 bp
* 92648 109897: contig of 17250 bp in length
* 109898 109997: gap of 100 bp
* 109998 127653: contig of 17656 bp in length
* 127654 127753: gap of 100 bp
* 127754 148735: contig of 20982 bp in length
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BASE COUNT 50061 a 34423 c 35174 g 50149 t 2213 others
ORIGIN

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Dp	96232	CACAGCTTACCGTGTACTTGGCCCTTATGTCACATGTTGGTAGTTC	TGGAACCTCTGTGA	96291
Qy	989	ACTCCTAGAGCTGAAAAAATTCAGAAAAATGTTCTATGTGAAGTAGAGACAGACAGAGA	1048	
Dp	96292	ACTCCTAGAGCTGAAAAAATTCAGAAAAATGTTCTATGTGAAGTAGAGACAGACAGAGA	96351	
Qy	1049	TCAGGTGCACATCATAGAGCATGAGCACTGCCTCCCTCCCTGATCCACAGACAGGCACGC	1108	
Dp	96352	TCAGGTGCACATCATAGAGCATGAGCACTGCCTCCCTCCCTGATCCACAGACAGGCACGC	96411	
Qy	1109	TGCGATGGAAGAGAGACACAGAAAGCAAAATGAGCCTTTTGGCCACCAAGTCATCTGCCTG	1168	
Dp	96412	TGCGATGGAAGAGAGACACAGAAAGCAAAATGAGCCTTTTGGCCACCAAGTCATCTGCCTG	96471	
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Qy	1229	GTCAGAGTGCAAGAGAGAGGCGTTAGTATGTTGTTCAATTTTATCATGATGCAAAAGGAGAAA	1288	
Dp	96532	GTCAGAGTGCAAGAGAGAGGCGTTAGTATGTTGTTCAATTTTATCATGATGCAAAAGGAGAAA	96591	
Qy	1289	TTATGTCACTTTTAAGAAATAGCTACTGTTTGGCAATGTCTTATTAACCAACCAAAAAA	1348	
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Dp	96712	TGTCACCTTAAATTCATATGTGACAAAAATTTCTCGACCTTAATAGAGAGAGATACT	96771	
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Dp	96892	AAAAAAGCATAGAGATGTTTAAATAGATTATGTTAGTATGAGGTTTGGATGACCC	96951	
Qy	1649	ACCCAAATATGATTTTGGAGAAATCTAAGTCAAACTCCTATTTATATCATAGGTA	1708	
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Dp	97012	ACCATTAAGTATGTCATATATAAGATATAATATGTTTATATCTGTACATATAGGTTTACG	97071	
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RESULT 7

AL360006

LOCUS

174629 bp

DNA

HTG

13-SEP-2000

DEFINITION	Homo sapiens chromosome 1 clone RP11-528D17, *** SEQUENCING IN PROGRESS ***; 15 unordered pieces.
ACCESSION	AL360006
VERSION	AL360006.5 GI:10178597
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 174629)
AUTHORS	Burton,J.
JOURNAL	Direct Submission Submitted (12-Sep-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk requests: lorna.requests@sanger.ac.uk On Sep 16, 2000 this sequence version replaced gi:9844026.
COMMENT	----- Genome Center  Center: Sanger Centre  Center code: SC Web site: http://www.sanger.ac.uk Contact: humquerry@sanger.ac.uk ----- Project Information Center project name: BA52BD17 ----- Summary Statistics  Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 167120 bases at least Q40 Consensus quality: 170054 bases at least Q30 Consensus quality: 171743 bases at least Q20 Insert size: 173229; sum-of-contigs Insert size: 185723; 5.5% error; agarose-fp Quality coverage: 4.45x in Q20 bases; sum-of-contigs Quality coverage: 4.21x in Q20 bases; agarose-fp ----- * NOTE: This is a 'working draft' sequence. It currently * consists of 15 contigs. The true order of the pieces * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved. * * 1      11804: contig of 11804 bp in length *      11805 11904: gap of        100 bp *      11905 16725: contig of 4821 bp in length *      16726 16825: gap of        100 bp *      16826 22352: contig of 8527 bp in length *      22353 25452: gap of        100 bp *      25453 65850: contig of 40398 bp in length *      65851 65950: gap of        100 bp *      65951 75623: contig of 9672 bp in length *      75623 75722: gap of        100 bp *      75723 85948: contig of 10221 bp in length *      85950 86049: gap of        100 bp *      86050 93827: contig of 7778 bp in length *      93828 93927: gap of        100 bp *      93928 102074: contig of 8147 bp in length *      102075 102174: gap of        100 bp *      102175 110564: contig of 8390 bp in length *      110565 110664: gap of        100 bp *      110665 132215: contig of 21551 bp in length *      132216 132315: gap of        100 bp *      132316 134650: contig of 2335 bp in length *      134651 134750: gap of        100 bp *      134751 152596: contig of 17846 bp in length *      152597 152696: gap of        100 bp *      152697 157665: contig of 4669 bp in length *      157666 157765: gap of        100 bp *      157766 161179: contig of 3414 bp in length *      161180 161279: gap of        100 bp *      161280 174629: contig of 13350 bp in length. * Location/Qualifiers
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Best Local Similarity 99.3%; Pred. No. 7.9e-126;
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 ACCESSION AF022819  
 VERSION AF022819.1 GI:4103371  
 KEYWORDS  
 SOURCE Norway rat.  
 ORGANISM Rattus norvegicus  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 REFERENCE 1 (bases 1 to 1582)  
 AUTHORS Gan, L., Joiner, W.J., Quinn, A.M., Wang, L.-Y., Hughes, T. and  
 Kaczmarek, L.K.  
 TITLE Cloning and localization of rTWIK, a putative potassium channel  
 with two P domains  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1582)

AUTHORS Gan, L., Joiner, W.J., Quinlan, A.M., Wang, L.-Y., Hughes, T. and

Kaczmarek, L.K.

TITLE Direct Submission

JOURNAL Submitted (05-SEP-1997) Cellular & Molecular Physiology, Yale

University, 333 Cedar St., New Haven, CT 06520, USA

FEATURES Location/Qualifiers

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CFISLTIGLYVGEYGNOKRELYKIGITNCYLLGLIAMIYVLETCCELKRF

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Best Local Similarity 85.6% Pred.No.2.1e-118:

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#### RESULT 9

AF004695

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

ADDITIONAL

TITLE

JOURNAL

REFERENCE

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*	8541	8640:	gap of	100	bp
*	8641	11132:	contlg of	2492	bp in length
*	11133	11232:	gap of	100	bp
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*	38132	38231:	gap of	100	bp
*	38232	44571:	contlg of	6340	bp in length
*	44572	44671:	gap of	100	bp
*	44672	50542:	contlg of	5871	bp in length
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*	60926	61025:	gap of	100	bp
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*	71075	71174:	gap of	100	bp
*	71175	82308:	contlg of	11134	bp in length
*	82309	82408:	gap of	100	bp
*	82409	92547:	contlg of	10139	bp in length
*	92548	92647:	gap of	100	bp
*	92648	109897:	contlg of	17250	bp in length
*	109898	109997:	gap of	100	bp
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*	127654	127753:	gap of	100	bp
*	127754	148735:	contlg of	20982	bp in length
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 alternatively spliced.  
 ACCESSION AF281304  
 VERSION AF281304.1 GI:9971948  
 KEYWORDS Norway rat.  
 SOURCE Rattus norvegicus  
 ORGANISM Rattus norvegicus  
 Chordata; Craniata; Vertebrata; Euteleostomi;  
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 REFERENCE 1 (bases 1 to 2243)  
 Patel,A.J., Malingret,F., Magnone,V., Fosset,M., Lazdunski,M. and  
 Honore,E.  
 TWIK-2, an inactivating 2P domain K+ channel  
 J. Biol. Chem. 275 (37), 28722-28730 (2000)  
 JOURNAL MEDLINE 20435832  
 REFERENCE 2 (bases 1 to 2243)  
 Patel,A.J., Malingret,F., Magnone,V., Fosset,M., Lazdunski,M. and  
 Honore,E.  
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 Submitted (23-JUN-2000) Institut de Pharmacologie Molculaire et  
 Cellulaire CNRS, 660, route des Lucioles, Valbonne 06560, France  
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 VERSION G20759.1 GI:1341096  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 REFERENCE 1 (bases 1 to 239)  
 AUTHORS Adams,M.D.  
 JOURNAL Unpublished (1996)  
 COMMENT

Contact: Mark Adams  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850  
 Email: mdadams@tigr.org

Primer A: GGTCTCTACTTCCACAT  
 Primer B: GCTCTGGAATTTTGTAT  
 STS size: 239

PCR Profile:  
 Denaturation: 96C 5min  
 Anneal: 54C 30sec  
 Extend: 72C 30sec  
 Denature: 95C 30sec  
 FinalExtend: 72C 5min  
 Cycles: 30

Protocol:  
 GenomicDNA: 25 ng  
 Primer: 0.43 uM each  
 dNTPs: 230 uM each  
 Amplifig: 0.5 units  
 Tagstart Ab: 0.5 units  
 Total Volume: 10 uL

Buffer: Tris-HCl pH8.8: 100 mM





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ACCESSION AX020359
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REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS   Little JOURNAL
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AUTHORS	Eutheria; Primates; Carnivora; Hominoidea; Homo.		
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